

#2

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in [BLASTN](#) program only:

Reward for a match: Penalty for a mismatch:

☐ Use [Mega BLAST](#) Strand option View option

Masking character option Masking color option

☐ Show CDS translation

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1

Enter accession, GI or sequence in FASTA format from: to:

```
gtgaacttttatgggaaggatgcttctgaaaaacaaatgacagaaaactctccgccaggg
gaatttttttctcaattttgatgaataagaacgatttgaaaatacaatggttgtgtttt
tatcttttttagagagctaaagggtgcctagaatctcttttcaaaaagcagattctctcatg
ttttttttctttatttgttgtcatattctttttacatcttctgaccacttatcctcaagt
tgtacctctcatgttttataatgacaagctggatcaacatgggaaaagggtgaactggca
gtgatttcaccagccctgacatccttgcattccaccagcgtgctcctttaagttcagccca
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from: to:

```
ctgcagcaagttacttaatgttttttgcctcagcatcctctctgtaaaatgagagcatta
gtcttgctccaacttcgagggcatggacagctctgggatttcatatccaagacccttaa
catcccacagtccttcccccaaacattctcctcctaataacctccctcagtttggtcag
gcctggaacaaaaaggcatacgaaatggtagaaaaagtgtccatgactactctgactta
gatgaagagaccaatgaaaatagtaatgactctgtttgcttcagcaggacatatactaaa
```

or upload FASTA file

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

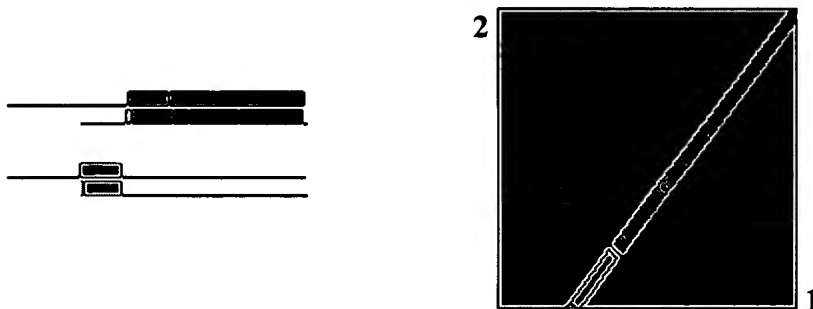
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lcl|1_seq_1
 Length = 2740 (1 .. 2740)

Sequence 2: lcl|2_seq_2
 Length = 2074 (1 .. 2074)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

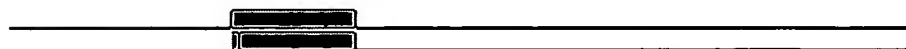


Score = 2878 bits (1497), Expect = 0.0
 Identities = 1613/1631 (98%), Gaps = 6/1631 (0%)
 Strand=Plus/Plus

Query	1110	GTGATAGCTGTGTCCATCTCAAAGAAAAGCCCAGGAGATTTCCCTTTAATTAACCCCTTT	1169
Sbjct	427	GTGATAGCTGTGTCCATCTCAAAGAAAAGCCCAGGAGATTTCCCTTTATTTACCCCTTT	484
Query	1170	TAAGATAGAATATTAGGAGACCGGAACATATGATACAGGAGGTACTGGGAGGGTCCCTCT	1229
Sbjct	485	TAAGATAGAATATTAGGAGACCGGAACATATGATACAGGAGGTACTGGGAGGGTCCCTCT	544
Query	1230	TTGTCAATGTTTGTCTTGGGGTGGGGAGTCGATGTCTTCTCAAAGTTTCAGAAACACCA	1289

Sbjct	545	TTGTCAATGTTTTGTCTTGGGGTGGGGAGTCGATGTCTTCTCAAAGTTTCAGAAACACCA	604
Query	1290	TCCACTGACTGAGCATTCAAGGGGCAAGAGGAGAATGGCAGCCACATTTGTTGATTGGGT	1349
Sbjct	605	TCCACTGACTGAGCATTCAAGGGGCAAGAGGAGAATGGCAGCCACATTTGTTGATTGGGT	664
Query	1350	GAGTTTGGGGAGAAATAGACACACAAAGGTCAAACATAACTTCCTAATTAAACACTTCCCT	1409
Sbjct	665	GAGTTTGGGGAGAAATAGACACACAAAGGTCAAACATAACTTCCTAATTAAACACTTCCCT	724
Query	1410	CCATTACACAATTCCTTCTCCCATTCTTCTCTCCTTTCTTTTACTGnnnnnnnnCCCAGTT	1469
Sbjct	725	CCATTACACAATTCCTTCTCCCATTCTTCTCTCCTGTCTTTTACTSAKARAAACCCAGTT	784
Query	1470	TTTCCTGAAACTATAAAAAATACCCC-AGTATTTTACATAAATTACACCTCAAAGATTAG	1528
Sbjct	785	TTTCCTGAAACTATAAAAAATACCCCAGTATGTTTACATAAATTACACCTCAAAGATTAG	844
Query	1529	AAACCAGAAATAGAGACCTTTTTCAACCCTTCCGGAAGCAAAGTGCATTATCCCTCCAGC	1588
Sbjct	845	AAACCAGAAATAGAGACCTTTT-CAACCCTTCCGGAAGCAAAGTGCATTATCCCTCCAGC	903
Query	1589	CACGTGTCTCAAATCTTGATGCATCAGAATCATCTGGGTGCTTTGAAATTCAAGATGATT	1648
Sbjct	904	CACGTGTCTCAAATCTTGATGCATCAGAATCATCTGGGTGCTTTKAAATTCAAGATGATT	963
Query	1649	CCTACGAGTTACCATAAATCAACTCAGAATTCCCTGGAGTGGGGCCAGGGATCTGTATT	1708
Sbjct	964	CCTACGAGTTACCATAAATCAACTCAGAATTCCCTGGAGTGGGGCC-AGGGATCTGTATT	1022
Query	1709	TCTGACAAGCTCCCACAGGTGATTCCCTTTCCCCACAGCATTTGAGAACTTCAGCTCAATG	1768
Sbjct	1023	TCTGACAAGCTCCCACAGGTGATTCCCTTTCCCCACAGCATTTGAGAACTTCAGCTCAATG	1082
Query	1769	ACCTAATCAGAGTCCTGCCATTGCTAATAACTGGTCTCAnnnnnnnnnCnnnnnnnnnnnnnn	1828
Sbjct	1083	ACCTAATCAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTTBTTCATATATATATATA	1142
Query	1829	GTATTTTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACTCCTAAGC	1888
Sbjct	1143	GTATTTGTTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACTCCTAAGC	1202
Query	1889	TAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGCCACTGCA	1948
Sbjct	1203	TAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGCCACTGCA	1262
Query	1949	CCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCATTTTGAAGT	2008
Sbjct	1263	CCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCATTTTGAAGT	1322
Query	2009	AAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCATGTGCTAATGGC	2068
Sbjct	1323	AAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCATGTGCTAATGGC	1382
Query	2069	CAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCTTTCAATTTCTTATAATGATGGT	2128
Sbjct	1383	CAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCTTTCAATGTCTTATAATGATGGT	1442
Query	2129	AAGGTGGCATGTCATGGGGCCTATTTAGCCCCAGACATCACTCCAAAGAATTCCAAACAG	2188

Sbjct	1443	AAGGTGGCATGTCATGGGGCCTATTTAGCCC-AGACATCACTCCAAAGAATTCCAAACAG	1501
Query	2189	ATATAGACAAGTGCCTTTAGGGCCCAGATCCCTTCCCCTCAGGCTGTTTACCCAGGGAAT	2248
Sbjct	1502	ATATAGACAAGTGCCTTTAGGGCCCAGATCCCTTCCCCTCAGGCTGTTTACCCAGGGAAT	1561
Query	2249	AGGATGTCCTGGGACAAGTTTCCCCTAAGTGAAGTGTGATAAGTCTGCATTATCAGAAAG	2308
Sbjct	1562	AGGATGTCCTGGGACAAGTTTCCCCTAAGTGAAGTGTGATAAGTCTGCATTATCAGAAAG	1621
Query	2309	ATATTACTGGGGGTGTGATATGTAGGGCATCTACATTTTCTTGATAGGTAGTCATATGAA	2368
Sbjct	1622	ATATTACTGGGGGTGTGATATGTAGGGCATCTACATTTTCTTGATAGGTAGTCATATGAA	1681
Query	2369	AGCTGACAAAGnnnnnnnnGGGCAGTGATGTGGTGCAATGTCAACAGACAGCTGTCCCCTG	2428
Sbjct	1682	AGCTGACAAAGAAAAAAGGGCAGTGATGTGGTGCAATGTCAACAGACAGCTGTCCCCTG	1741
Query	2429	ACTCTTGACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGG	2488
Sbjct	1742	ACTCTTGACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGG	1801
Query	2489	CCCTCTCACATTTCTTCTGATTACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCCT	2548
Sbjct	1802	CCCTCTCACATTTCTTCTGATTACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCCT	1861
Query	2549	CTTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCT	2608
Sbjct	1862	CTTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCT	1921
Query	2609	AATGGGGGCGGGAGTGTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAG	2668
Sbjct	1922	AATGGGGGCGGGAGTGTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAG	1981
Query	2669	CTATATAAGCTGACCGGTGTGGAGGGGCCAGCAGGGCCAACCTCCAGGGATTCTTCCAC	2728
Sbjct	1982	CTATATAAGCTGACCGGTGTGGAGGGGCCAGCAGGGCCAACCTCCAGGGATTCTTCCAC	2041
Query	2729	GACAGAAAAAC 2739	
Sbjct	2042	GACAGAAAAAC 2052	



Score = 710 bits (369), Expect = 0.0
Identities = 376/377 (99%), Gaps = 1/377 (0%)
Strand=Plus/Plus

Query	683	CTGCAGCAAGTTACTTAAATGTTTCTTTGCCCTCAGCATCCTCTCTGTAAAATGAGAGCATT	742
Sbjct	1	CTGCAGCAAGTTACTTAAATGTTT-TTTGCCCTCAGCATCCTCTCTGTAAAATGAGAGCATT	59
Query	743	AGTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTTCATATCCAAGACCCTTAA	802
Sbjct	60	AGTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTTCATATCCAAGACCCTTAA	119

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Query   803   ACATCCCACAGTCCTTCCCCCAAACACTTCTCCTCCTAATACCTCCCTCAGTTTGGGTCA   862
          |||
Sbjct   120   ACATCCCACAGTCCTTCCCCCAAACACTTCTCCTCCTAATACCTCCCTCAGTTTGGGTCA   179

Query   863   GGCCTGGAACAAAAAGGCATACGAAATGGTAGAAAAAGTGTCATGACTACTTCTGACTT   922
          |||
Sbjct   180   GGCCTGGAACAAAAAGGCATACGAAATGGTAGAAAAAGTGTCATGACTACTTCTGACTT   239

Query   923   AGATGAAGAGACCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAA   982
          |||
Sbjct   240   AGATGAAGAGACCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAA   299

Query   983   AATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTG   1042
          |||
Sbjct   300   AATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTG   359

Query   1043  TGAAACATTCCATATAT   1059
          |||
Sbjct   360   TGAAACATTCCATATAT   376

```

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H
1.33 0.621 1.12

Gapped

Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Sequences: 1
 Number of Hits to DB: 556
 Number of extensions: 13
 Number of successful extensions: 9
 Number of sequences better than 10.0: 1
 Number of HSP's gapped: 2
 Number of HSP's successfully gapped: 2
 Length of query: 2740
 Length of database: 18,279,132,206
 Length adjustment: 27
 Effective length of query: 2713
 Effective length of database: 18,279,132,179
 Effective search space: 49591285601627
 Effective search space used: 49591285601627
 X1: 11 (21.1 bits)
 X2: 26 (50.0 bits)
 X3: 26 (50.0 bits)
 S1: 14 (27.6 bits)
 S2: 22 (43.0 bits)